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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/852,370

DATE: 06/14/2001

TIME: 11:57:01

Input Set : N:\Crf3\RULE60\09852370.txt

Output Set: N:\CRF3\06142001\I852370.raw

ENTERED

3 <110> APPLICANT: Pomerantz, Joel L.  
4 Sharp, Phillip A.  
5 Pabo, Carl O.  
7 <120> TITLE OF INVENTION: Chimeric DNA-binding proteins  
9 <130> FILE REFERENCE: APV-022.02  
12 <140> CURRENT APPLICATION NUMBER: 09/852,370  
13 <141> CURRENT FILING DATE: 2001-05-10  
15 <150> PRIOR APPLICATION NUMBER: 08/973,131  
16 <151> PRIOR FILING DATE: 1997-11-26  
18 <150> PRIOR APPLICATION NUMBER: PCT/US95/16982  
19 <151> PRIOR FILING DATE: 1995-12-29  
21 <150> PRIOR APPLICATION NUMBER: 08/366,083  
22 <151> PRIOR FILING DATE: 1994-12-29  
24 <160> NUMBER OF SEQ ID NOS: 75  
26 <170> SOFTWARE: PatentIn Ver. 2.0  
28 <210> SEQ ID NO: 1  
29 <211> LENGTH: 26  
30 <212> TYPE: DNA  
31 <213> ORGANISM: Artificial Sequence  
33 <220> FEATURE:  
34 <223> OTHER INFORMATION: Description of Artificial Sequence:  
35 oligonucleotide used to determine the consensus  
36 binding sequence of ZFHD1  
38 <400> SEQUENCE: 1  
39 gtttggcacc tgactaattt aaggag 26  
42 <210> SEQ ID NO: 2  
43 <211> LENGTH: 25  
44 <212> TYPE: DNA  
45 <213> ORGANISM: Artificial Sequence  
47 <220> FEATURE:  
48 <223> OTHER INFORMATION: Description of Artificial Sequence:  
49 oligonucleotide used to determine the consensus  
50 binding sequence of ZFHD1  
52 <400> SEQUENCE: 2  
53 gcgttaatta agggaggtaa ggccc 25  
56 <210> SEQ ID NO: 3  
57 <211> LENGTH: 25  
58 <212> TYPE: DNA  
59 <213> ORGANISM: Artificial Sequence  
61 <220> FEATURE:  
62 <223> OTHER INFORMATION: Description of Artificial Sequence:  
63 oligonucleotide used to determine the consensus  
64 binding sequence of ZFHD1  
66 <400> SEQUENCE: 3  
67 ctcgcccggtt aatgaggggt gttcg 25  
70 <210> SEQ ID NO: 4  
71 <211> LENGTH: 25

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72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <223> OTHER INFORMATION: Description of Artificial Sequence:
77     oligonucleotide used to determine the consensus
78     binding sequence of ZFHD1
80 <400> SEQUENCE: 4
81 taattatggg cgggatcgaa tagcc                25
84 <210> SEQ ID NO: 5
85 <211> LENGTH: 26
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: Description of Artificial Sequence:
91     oligonucleotide used to determine the consensus
92     binding sequence of ZFHD1
94 <400> SEQUENCE: 5
95 ggcaataatc aatcctttaa ttatgg                26
98 <210> SEQ ID NO: 6
99 <211> LENGTH: 26
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Description of Artificial Sequence:
105     oligonucleotide used to determine the consensus
106     binding sequence of ZFHD1
108 <400> SEQUENCE: 6
109 ggccgtacct catgaaatta ggggcg                26
112 <210> SEQ ID NO: 7
113 <211> LENGTH: 25
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Artificial Sequence:
119     oligonucleotide used to determine the consensus
120     binding sequence of ZFHD1
122 <400> SEQUENCE: 7
123 gttaattatg gggtaataat ggtgc                25
126 <210> SEQ ID NO: 8
127 <211> LENGTH: 25
128 <212> TYPE: DNA
129 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:
132 <223> OTHER INFORMATION: Description of Artificial Sequence:
133     oligonucleotide used to determine the consensus
134     binding sequence of ZFHD1
136 <400> SEQUENCE: 8
137 gtcgggctct gttaattatg ggtgg                25
140 <210> SEQ ID NO: 9

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141 <211> LENGTH: 25
142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: Description of Artificial Sequence:
147     oligonucleotide used to determine the consensus
148     binding sequence of ZFHD1
150 <400> SEQUENCE: 9
151 ggataattac ggggtggcatt taggc                25
154 <210> SEQ ID NO: 10
155 <211> LENGTH: 25
156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Description of Artificial Sequence:
161     oligonucleotide used to determine the consensus
162     binding sequence of ZFHD1
164 <400> SEQUENCE: 10
165 gataaatagg ggcgtcccat cccgt                25
168 <210> SEQ ID NO: 11
169 <211> LENGTH: 24
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence:
175     oligonucleotide used to determine the consensus
176     binding sequence of ZFHD1
178 <400> SEQUENCE: 11
179 taaattaggg ctttaattac ggtc                24
182 <210> SEQ ID NO: 12
183 <211> LENGTH: 25
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Description of Artificial Sequence:
189     oligonucleotide used to determine the consensus
190     binding sequence of ZFHD1
192 <400> SEQUENCE: 12
193 tcattagagt gttaatgaga tgcgc                25
196 <210> SEQ ID NO: 13
197 <211> LENGTH: 26
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: Description of Artificial Sequence:
203     oligonucleotide used to determine the consensus
204     binding sequence of ZFHD1
206 <400> SEQUENCE: 13
207 tagttgctaa tttgtattaa ttaaag                26

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Input Set : N:\Crf3\RULE60\09852370.txt

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210 <210> SEQ ID NO: 14
211 <211> LENGTH: 25
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213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Description of Artificial Sequence:
217     oligonucleotide used to determine the consensus
218     binding sequence of ZFHD1
220 <400> SEQUENCE: 14
221 agttattaat taagaatggt aatta                25
224 <210> SEQ ID NO: 15
225 <211> LENGTH: 25
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Description of Artificial Sequence:
231     oligonucleotide used to determine the consensus
232     binding sequence of ZFHD1
234 <400> SEQUENCE: 15
235 gtgtgataat gagctgggcc gtccc                25
238 <210> SEQ ID NO: 16
239 <211> LENGTH: 25
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Description of Artificial Sequence:
245     oligonucleotide used to determine the consensus
246     binding sequence of ZFHD1
248 <400> SEQUENCE: 16
249 atattaaggc gtaattcgga caaga                25
252 <210> SEQ ID NO: 17
253 <211> LENGTH: 12
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: consensus
259     binding sequence of ZFHD1
261 <220> FEATURE:
262 <223> OTHER INFORMATION: "n" represents a, t, c, g or other
264 <400> SEQUENCE: 17
W--> 265 taattanggg ng                12
268 <210> SEQ ID NO: 18
269 <211> LENGTH: 12
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Description of Artificial Sequence: hybrid DNA
275     site
277 <220> FEATURE:

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DATE: 06/14/2001

PATENT APPLICATION: US/09/852,370

TIME: 11:57:01

Input Set : N:\Crif3\RULE60\09852370.txt

Output Set: N:\CRF3\06142001\I852370.raw

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278 <223> OTHER INFORMATION: "n" represents a, t, c, g or other
280 <400> SEQUENCE: 18
W--> 281 aaatnntggg cg 12
284 <210> SEQ ID NO: 19
285 <211> LENGTH: 12
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Description of Artificial Sequence: predicted
291 binding sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: "n" represents a, t, c, g or other
296 <400> SEQUENCE: 19
W--> 297 cgcccannaa at 12
300 <210> SEQ ID NO: 20
301 <211> LENGTH: 10
302 <212> TYPE: DNA
303 <213> ORGANISM: human
305 <400> SEQUENCE: 20
306 atgcaaata 10
309 <210> SEQ ID NO: 21
310 <211> LENGTH: 12
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Description of Artificial Sequence: hybrid binding
316 site
318 <400> SEQUENCE: 21
319 taatgatggg cg 12
322 <210> SEQ ID NO: 22
323 <211> LENGTH: 63
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
328 <223> OTHER INFORMATION: Description of Artificial Sequence: hybrid binding
329 site
331 <220> FEATURE:
332 <223> OTHER INFORMATION: "n" represents a, t, c, g or other
334 <400> SEQUENCE: 22
W--> 335 ggctgagtct gaacggatcc nnnnnnnnnn nnnnnnnnnn nnnnnccctcg agactgagcg 60
337 tcg 63
340 <210> SEQ ID NO: 23
341 <211> LENGTH: 12
342 <212> TYPE: DNA
343 <213> ORGANISM: Artificial Sequence
345 <220> FEATURE:
346 <223> OTHER INFORMATION: Description of Artificial Sequence: probe
348 <400> SEQUENCE: 23
349 tcattatggg cg 12

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## VERIFICATION SUMMARY

DATE: 06/14/2001

PATENT APPLICATION: US/09/852,370

TIME: 11:57:02

Input Set : N:\Crf3\RULE60\09852370.txt

Output Set: N:\CRF3\06142001\I852370.raw

L:265 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17  
L:265 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17  
L:265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:281 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18  
L:281 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18  
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:297 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19  
L:297 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19  
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:335 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22  
L:335 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22  
L:335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:657 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:657 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:841 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:841 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:869 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:869 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:908 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:908 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: